

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/119,209

DATE: 07/24/98
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INPUT SET: S27686.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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98 NOV 18 AM 11:45
GROUP 180

SEQUENCE LISTING

- 1
- 2
- 3 (1) General Information:
- 4
- 5 (i) APPLICANT: LASKY, LAURENCE A.
- 6 STACHELL, SCOTT E.
- 7 ROSEN, STEVEN D.
- 8 SINGER, MARK S.
- 9 YEDNOCK, TED A.
- 10
- 11 (ii) TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
- 12
- 13 (iii) NUMBER OF SEQUENCES: 6
- 14
- 15 (iv) CORRESPONDENCE ADDRESS:
- 16 (A) ADDRESSEE: Genentech, Inc.
- 17 (B) STREET: 1 DNA Way
- 18 (C) CITY: South San Francisco
- 19 (D) STATE: California
- 20 (E) COUNTRY: USA
- 21 (F) ZIP: 94080
- 22
- 23 (v) COMPUTER READABLE FORM:
- 24 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- 25 (B) COMPUTER: IBM PC compatible
- 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 27 (D) SOFTWARE: WinPatin (Genentech)
- 28
- 29 (vi) CURRENT APPLICATION DATA:
- 30 (A) APPLICATION NUMBER:
- 31 (B) FILING DATE: 20-Jul-1998
- 32 (C) CLASSIFICATION:
- 33
- 34 (vii) PRIOR APPLICATION DATA:
- 35 (A) APPLICATION NUMBER: 08/513278
- 36 (B) FILING DATE: 10-AUG-1995
- 37
- 38 (vii) PRIOR APPLICATION DATA:
- 39 (A) APPLICATION NUMBER: 08/059027
- 40 (B) FILING DATE: 6-MAY-1993
- 41
- 42 (vii) PRIOR APPLICATION DATA:
- 43 (A) APPLICATION NUMBER: 07/786149
- 44 (B) FILING DATE: 31-OCT-1991
- 45
- 46 (vii) PRIOR APPLICATION DATA:

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PATENT APPLICATION US/09/119,209DATE: 07/24/98
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47 (A) APPLICATION NUMBER: 07/315015
48 (B) FILING DATE: 23-FEB-1989
49
50 (viii) ATTORNEY/AGENT INFORMATION:
51 (A) NAME: Love, Richard B.
52 (B) REGISTRATION NUMBER: 34,659
53 (C) REFERENCE/DOCKET NUMBER: P0565D1C3
54
55 (ix) TELECOMMUNICATION INFORMATION:
56 (A) TELEPHONE: 650/225-5530
57 (B) TELEFAX: 650/952-9881
58 (2) INFORMATION FOR SEQ ID NO:1:
59
60 (i) SEQUENCE CHARACTERISTICS:
61 (A) LENGTH: 2259 base pairs
62 (B) TYPE: Nucleic Acid
63 (C) STRANDEDNESS: Single
64 (D) TOPOLOGY: Linear
65
66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
67
68
69 GAATTCCAGT GTGCTGGCTT CCTCACCTGC AGCACAGCAC ACTCCCTTTG 50
70
71 GCAAGGACCT GAGACCCTTG TGCTAAGTCA AGAGGCTCAA TGGGCTGCAG 100
72
73 AAGAACTAGA GAAGGACCAA GCAAAGCCAT GATATTTCCA TGGAAATGTC 150
74
75 AGAGCACCCA GAGGGACTTA TGGAACATCT TCAAGTTGTG GGGGTGGACA 200
76
77 ATGCTCTGTT GTGATTTCCCT GGCACATCAT GGAACCTACT GCTGGACTTA 250
78
79 CCATTATTCT GAAAAACCCA TGAAGTGGCA AAGGGCTAGA AGATTCTGCC 300
80
81 GAGACAATTA CACAGATTTA GTTGCCATAC AAAACAAGGC GGAAATTGAG 350
82
83 TATCTGGAGA AGACTCTGCC CTTCACTCGT TCTTACTACT GGATAGGAAT 400
84
85 CCGGAAGATA GGAGGAATAT GGACGTGGGT GGGAACCAAC AAATCTCTCA 450
86
87 CTGAAGAAGC AGAGAACTGG GGAGATGGTG AGCCCAACAA CAAGAAGAAC 500
88
89 AAGGAGGACT GCGTGGAGAT CTATATCAAG AGAAACAAAG ATGCAGGCAA 550
90
91 ATGGAACGAT GACGCCTGCC ACAAATAAAA GGCAGCCCTC TGTTACACAG 600
92
93 CTTCTTGCCA GCCCTGGTCA TGCAGTGGCC ATGGAGAATG TGTAAGAAATC 650
94
95 ATCAATAATC ACACCTGCAA CTGTGATGTG GGGTACTATG GGCCCCAGTG 700
96
97 TCAGCTTGTG ATTCAGTGTG AGCCTTTGGA GGCCCCAGAG CTGGGTACCA 750
98
99 TGGACTGTAC TCACCCCTTT GGAAACTTCA GCTTCAGCTC ACAGTGTGCC 800

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100
101 TTCAGCTGCT CTGAAGGAAC AAACCTTAACT GGGATTGAAG AAACCACCTG 850
102
103 TGGACCATTT GGAAACTGGT CATCTCCAGA ACCAACCTGT CAAGTGATTC 900
104
105 AGTGTGAGCC TCTATCAGCA CCAGATTTGG GGATCATGAA CTGTAGCCAT 950
106
107 CCCCTGGCCA GCTTCAGCTT TACCTCTGCA TGTACCTTCA TCTGCTCAGA 1000
108
109 AGGAACTGAG TTAATTGGGA AGAAGAAAAC CATTTGTGAA TCATCTGGAA 1050
110
111 TCTGGTCAAA TCCTAGTCCA ATATGTCAAA AATTGGACAA AAGTTTCTCA 1100
112
113 ATGATTAAAGG AGGGTGATTA TAACCCCTC TTCATTCCAG TGGCAGTCAT 1150
114
115 GGTTACTGCA TTCTCTGGGT TGGCATTAT CATTTGGCTG GCAAGGAGAT 1200
116
117 TAAAAAAGG CAAGAAATCC AAGAGAAGTA TGAATGACCC ATATTAAATC 1250
118
119 GCCCTTGGTG AAAGAAAAT CTTGGAATAC TAAAAATCAT GAGATCCTTT 1300
120
121 AAATCCTTCC ATGAAACGTT TTGTGTGGTG GCACCTCCTA CGTCAAACAT 1350
122
123 GAAGTGTGTT CCTTCAGTGC ATCTGGGAAG ATTTCTACCC GACCAACAGT 1400
124
125 TCCTTCAGCT TCCATTTTCG CCCTCATTTA TCCCTCAACC CCCAGCCCAC 1450
126
127 AGGTGTTTAT ACAGCTCAGC TTTTGTCTT TTCTGAGGAG AAACAAATAA 1500
128
129 GACCATAAGG GAAAGGATTC ATGTGGAATA TAAAGATGGC TGAATTTGCT 1550
130
131 CTTTCTTGAC TCTTGTTTTC AGTTTCAATT CAGTGCTGTA CTTGATGACA 1600
132
133 GACACTTCTA AATGAAGTGC AAATTTGATA CATATGTGAA TATGGACTCA 1650
134
135 GTTTTCTTGC AGATCAAATT TCACGTCGTC TTCTGTATAC TGTGGAGGTA 1700
136
137 CACTCTTATA GAAAGTTCAA AAAGTCTACG CTCTCCTTTC TTTCTAACTC 1750
138
139 CAGTGAAGTA ATGGGGTCCT GCTCAAGTTG AAAGAGTCCT ATTTGCACTG 1800
140
141 TAGCCTCGCC GTCTGTGAAT TGGACCATCC TATTTAACTG GCTTCAGGCC 1850
142
143 TCCCCACCTT CTTCAGCCAC CTCTCTTTT CAGTTGGCTG ACTTCCACAC 1900
144
145 CTAGCATCTC ATGAGTGCCA AGCAAAAGGA GAGAAGAGAG AAATAGCCTG 1950
146
147 CGCGGTTTTT TAGTTTGGGG GTTTTGCTGT TTCCTTTAT GAGACCCATT 2000
148
149 CCTATTTCTT ATAGTCAATG TTTCTTTTAT CACGATATTA TTAGTAAGAA 2050
150
151 AACATCACTG AAATGCTAGC TGCAAGTGAC ATCTCTTTGA TGTCATATGG 2100
152

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153 AAGAGTTAAA ACAGGTGGAG AAATTCCTTG ATTCACAATG AAATGCTCTC 2150
154
155 CTTTCCCCTG CCCCCAGAAC TTTTATCCAC TTACCTAGAT TCTACATATT 2200
156
157 CTTTAAATTT CATCTCAGGC CTCCCTCAAC CCCACGGGGC CGCCAGCACA 2250
158
159 CTGGAATTC 2259
160

161 (2) INFORMATION FOR SEQ ID NO:2:

162
163 (i) SEQUENCE CHARACTERISTICS:
164 (A) LENGTH: 372 amino acids
165 (B) TYPE: Amino Acid
166 (D) TOPOLOGY: Linear
167

168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

169
170 Met Ile Phe Pro Trp Lys Cys Gln Ser Thr Gln Arg Asp Leu Trp
171 1 5 10 15
172
173 Asn Ile Phe Lys Leu Trp Gly Trp Thr Met Leu Cys Cys Asp Phe
174 20 25 30
175
176 Leu Ala His His Gly Thr Tyr Cys Trp Thr Tyr His Tyr Ser Glu
177 35 40 45
178
179 Lys Pro Met Asn Trp Gln Arg Ala Arg Arg Phe Cys Arg Asp Asn
180 50 55 60
181
182 Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Ala Glu Ile Glu Tyr
183 65 70 75
184
185 Leu Glu Lys Thr Leu Pro Phe Ser Arg Ser Tyr Tyr Trp Ile Gly
186 80 85 90
187
188 Ile Arg Lys Ile Gly Gly Ile Trp Thr Trp Val Gly Thr Asn Lys
189 95 100 105
190
191 Ser Leu Thr Glu Glu Ala Glu Asn Trp Gly Asp Gly Glu Pro Asn
192 110 115 120
193
194 Asn Lys Lys Asn Lys Glu Asp Cys Val Glu Ile Tyr Ile Lys Arg
195 125 130 135
196
197 Asn Lys Asp Ala Gly Lys Trp Asn Asp Asp Ala Cys His Lys Leu
198 140 145 150
199
200 Lys Ala Ala Leu Cys Tyr Thr Ala Ser Cys Gln Pro Trp Ser Cys
201 155 160 165
202
203 Ser Gly His Gly Glu Cys Val Glu Ile Ile Asn Asn His Thr Cys
204 170 175 180
205

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206	Asn Cys Asp Val Gly Tyr Tyr Gly Pro Gln Cys Gln Leu Val Ile	
207	185	190 195
208		
209	Gln Cys Glu Pro Leu Glu Ala Pro Glu Leu Gly Thr Met Asp Cys	
210	200	205 210
211		
212	Thr His Pro Phe Gly Asn Phe Ser Phe Ser Ser Gln Cys Ala Phe	
213	215	220 225
214		
215	Ser Cys Ser Glu Gly Thr Asn Leu Thr Gly Ile Glu Glu Thr Thr	
216	230	235 240
217		
218	Cys Gly Pro Phe Gly Asn Trp Ser Ser Pro Glu Pro Thr Cys Gln	
219	245	250 255
220		
221	Val Ile Gln Cys Glu Pro Leu Ser Ala Pro Asp Leu Gly Ile Met	
222	260	265 270
223		
224	Asn Cys Ser His Pro Leu Ala Ser Phe Ser Phe Thr Ser Ala Cys	
225	275	280 285
226		
227	Thr Phe Ile Cys Ser Glu Gly Thr Glu Leu Ile Gly Lys Lys Lys	
228	290	295 300
229		
230	Thr Ile Cys Glu Ser Ser Gly Ile Trp Ser Asn Pro Ser Pro Ile	
231	305	310 315
232		
233	Cys Gln Lys Leu Asp Lys Ser Phe Ser Met Ile Lys Glu Gly Asp	
234	320	325 330
235		
236	Tyr Asn Pro Leu Phe Ile Pro Val Ala Val Met Val Thr Ala Phe	
237	335	340 345
238		
239	Ser Gly Leu Ala Phe Ile Ile Trp Leu Ala Arg Arg Leu Lys Lys	
240	350	355 360
241		
242	Gly Lys Lys Ser Lys Arg Ser Met Asn Asp Pro Tyr	
243	365	370 372
244		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2214 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCTCGA GCTCGTCGAC CACGCCCTCC TTGTGCAAGA ACTCTGAGCC 50
CCAGGTGCAG GAGGCTGAGG CCTGCAGAGA GACTTGCAGA GAGACCCAGC 100

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SEQUENCE VERIFICATION REPORT
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